

08/476567
 attachment to
 Page # 15

MASPAR (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Aug 8 16:02:47 1997; MasPar time 1175.28 Seconds
 1326.024 Million cell updates/sec

Tabular output not generated.

Title: >N70819
 Description: (1-1419) from us08476567.seq
 Perfect Score: 1419
 N.A. Sequence: 1 ccgagccgagaatgggagta.....aatagaggagtcaagttcctt 1419
 Comp: ggctcggtctcttaccctcat.....ttatctcctcagttcaagaa

Scoring table: TABLE default
 Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 362067 seqs, 549138275 bases x 2

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: emb1-new3
 1:BCT 2:FUN 3:GEN1 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV
 9:ORG 10:MAM 11:VRT 12:PLN 13:PRO 14:ROD 15:SYN 16:UNC
 17:VIR

Database: genbank99
 18:BCT1 19:BCT2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 24:BCT7
 25:BCT8 26:BCT9 27:BCT10 28:BCT11 29:GEN1 30:GEN2
 31:GEN3 32:HTG1 33:HTG2 34:HTG3 35:INV1 36:INV2 37:INV3
 38:INV4 39:INV5 40:INV6 41:INV7 42:INV8 43:INV9 44:INV10
 45:INV11 46:MAM1 47:MAM2 48:MAM3 49:VRT1 50:VRT2 51:VRT3
 52:VRT4 53:PAT1 54:PAT2 55:PAT3 56:PAT4 57:PAT5 58:PHG
 59:PLN1 60:PLN2 61:PLN3 62:PLN4 63:PLN5 64:PLN6 65:PLN7
 66:PLN8 67:PLN9 68:PLN10 69:PLN11 70:PRI1 71:PRI2
 72:PRI3 73:PRI4 74:PRI5 75:PRI6 76:PRI7 77:PRI8 78:PRI9
 79:PRI10 80:PRI11 81:PRI12 82:PRI13 83:PRI14 84:PRI15
 85:ROD1 86:ROD2 87:ROD3 88:ROD4 89:ROD5 90:ROD6 91:ROD7
 92:ROD8 93:STR 94:SYN 95:UNA 96:VRL1 97:VRL2 98:VRL3
 99:VRL4 100:VRL5 101:VRL6 102:VRL7 103:VRL8 104:VRL9
 105:VRL10

Database: genbank-new3
 106:BCT 107:GEN1 108:GEN2 109:HTG1 110:HTG2 111:INV
 112:MAM 113:VRT 114:PHG 115:PLN 116:PRI1 117:PRI2
 118:ROD 119:SYN 120:UNA 121:VRL

Database: u-emb150_99
 122:part1

Statistics: Mean 11.369; Variance 4.112; scale 2.765

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match Length	DB	ID	Description	Pred. No.	

1	1419	100.0	1419	53	A12480	cDNA for glutamine sy	0.00e+00
2	1419	100.0	1421	85	CLGSR	Chinese hamster mRNA	0.00e+00
3	1003	70.7	2731	85	MMGSASE	M.musculus mRNA for g	0.00e+00
4	943	66.5	1150	86	MMU09114	Mus musculus glutamat	0.00e+00
5	926	65.3	2787	92	RRGS	Rat mRNA for glutamin	0.00e+00
6	926	65.3	2787	90	RATGLUS	R.norvegicus glutamin	0.00e+00
7	921	64.9	1366	74	HSGLUSYN	Human mRNA for glutam	0.00e+00
8	919	64.8	2727	74	HSGLUS	Human rearranged mRNA	0.00e+00
9	917	64.6	2793	90	RATGLNAB	Rat glutamine synthet	0.00e+00
10	911	64.2	2631	84	S70290	glutamine synthetase	0.00e+00
11	898	63.3	1370	48	SSGLUSYN	S.scrofa mRNA for glu	0.00e+00
12	881	62.1	2925	88	MUSGSA	Mouse intronless glut	0.00e+00
13	812	57.2	3004	77	HSU08626	Human glutamine synth	0.00e+00
14	673	47.4	1838	51	S45408	glutamine synthetase	0.00e+00
15	671	47.3	2728	49	CHKGLN	Chicken retinal gluta	0.00e+00
16	572	40.3	2753	51	SAU04617	Squalus acanthias glu	0.00e+00
17	450	31.7	1617	52	XELXGS	Xenopus laevis mRNA f	0.00e+00
18	449	31.6	1851	88	MUSGLN1	Mouse glutamine synth	0.00e+00
19	342	24.1	2935	43	PALGLUSYN	Paracentrotus lividus	0.00e+00
20	299	21.1	2045	44	PNLGTSYN	Panulirus argus gluta	3.85e-298
21	251	17.7	386	46	BOVGLN	Bovine glutamine synt	8.10e-243
22	247	17.4	2371	90	RATGLUSG6	Rat glutamine synthet	3.15e-238
23	218	15.4	1496	39	DMGS2	D.melanogaster GS2 mR	4.68e-205
24	192	13.5	2162	39	DMGS1	D.melanogaster GS1 mR	1.63e-175
25	181	12.8	649	90	RATGLUSG5	Rat glutamine synthet	4.39e-163
26	172	12.1	2424	60	COGGLN	Colletotrichum gloeos	5.97e-153
27	145	10.2	1354	60	BNGLN	B.napus mRNA for glut	8.77e-123
28	145	10.2	1780	69	YSCGLN1	S.cerevisiae glutamin	8.77e-123
29	145	10.2	10339	65	SC3085	S.cerevisiae chromoso	8.77e-123
30	145	10.2	165536	65	SCCHRXVI	S.cerevisiae chromoso	8.77e-123
31	143	10.1	1450	65	S46513	cytosolic glutamine s	1.45e-120
32	142	10.0	387	90	RATGLUSG2	Rat glutamine synthet	1.86e-119
33	136	9.6	1326	64	RADGS1GC	Raphanus sativus mRNA	8.02e-113
34	136	9.6	1429	63	LSGLUSYN	L.sativa mRNA for glu	8.02e-113
35	135	9.5	1440	62	LJCYTGLSY	L.japonica mRNA for c	1.02e-111
36	134	9.4	1317	69	ZMGS13	Z.mays mRNA gsl-3 for	1.29e-110
37	134	9.4	1490	69	ZMGS14	Z.mays mRNA gsl-4 for	1.29e-110
38	132	9.3	1332	64	PSGSISO	P.sylvestris mRNA for	2.06e-108
39	132	9.3	1350	63	MZEGS1B	Maize mRNA for glutam	2.06e-108
40	132	9.3	1422	63	MZEGS1A	Maize mRNA for glutam	2.06e-108
41	131	9.2	1484	64	RADGS1BB	Raphanus sativus mRNA	2.60e-107
42	130	9.2	1553	63	OSSIGS28	Oryza sativa shoot GS	3.27e-106
43	131	9.2	1649	63	OSSIGS31	Oryza sativa shoot GS	2.60e-107
44	129	9.1	1454	64	PVGSR1	Phaseolus vulgaris mR	4.10e-105
45	129	9.1	1483	69	ZMGS2	Z.mays mRNA gs2 for g	4.10e-105

ALIGNMENTS

```

RESULT      1
LOCUS       A12480      1419 bp    RNA          PAT      09-DEC-1993
DEFINITION  cDNA for glutamine synthatase.
ACCESSION  A12480
NID        g490275
KEYWORDS    .
SOURCE      long-tailed hamster.
  ORGANISM  Cricetulus longicaudatus
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
            Cricetinae; Cricetulus.
REFERENCE  1 (bases 1 to 1419)
AUTHORS    .
TITLE      RECOMBINANT DNA SEQUENCES, VECTORS CONTAINING THEM AND METHOD FOR
            THE USE THEREOF
JOURNAL    Patent: WO 8704462-A 1 30-JUL-1987;

FEATURES             Location/Qualifiers
     source            1..1419
                       /organism="Cricetulus longicaudatus"
     CDS               145..1266
                       /gene="GS gene"
                       /codon_start=1
                       /db_xref="PID:g490276"
                       /db_xref="SWISS-PROT:P04773"

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Db 270 ggaactttgatggctccagcaccttccaagccgaaggctccaacagcgacatgtacctgc 329
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Qy 323 ggaattttgatggctctagtacctttcagtcctgagggctccaacagtgacatgtatctca 382

Db 330 gacctgtgcatgtttccgggaccttttcgcaaggatcccaacaaattagttctctgtg 389
    |||| |||||||| |||||| || |||||| || || |||||| ||
Qy 383 gcctgttgcatgtttccgggaccttccgcagagatcccaacaagctgggtctctgtg 442

Db 390 aggtcttcaaatacaaccgccagtcctgcagacacaaatcttcggcacacctgtaggcgga 449
    |||| |||||| |||||| || |||||| || || |||||| ||
Qy 443 aagttttcaagtacaaccggaagcctgcagagaccaatttaaggcactcgtgtaaacgga 502

Db 450 ttatggatatgggtccaaccagcaccctggtttgggatggagcaggagtacacccttc 509
    |||| |||||| |||||| || |||||| || || |||||| ||
Qy 503 taatggacatgggtgagcaaccagcaccctggtttggaatggaacaggagtatactctga 562

Db 510 tgggaacagatggcatccgttttggtggccttccaattgcttccctggaccccaaggtc 569
    |||| |||||| || || |||||| || || |||||| ||
Qy 563 tgggaacagatgggcacccttttggttgcccttccaattgcttccctgggcccccaaggtc 622

Db 570 cgtactactgcggtgtaggagctgacaaagcctatggcagagacattgtggaggccact 629
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Qy 623 cgtattactgtggtgtgggcgcagacaaagcctatggcagggatctcgtggaggctcact 682

Db 630 accgagcgtgcctgtatgctggtgtgaaaattggaggaaccaacgcagaagtgtgccag 689
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Qy 683 accgcgcctgcttgtatgctgggtcaagattacaggaacaaatgctgaggtcatgcctg 742

Db 690 cccagtgaggagtccaggtgggacctgccaagggattgagatgggggatcacctctgga 749
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Qy 743 cccagtggaattccaaataggacctgtgaaggaatccgcagggagatcatctctggg 802

Db 750 tagcacgtttcactcctccacccgggtgtgccaagacttttggtgtcattgtgtccttcgatc 809
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Qy 803 tggcccggttcatcttgcatcgagtatgtgaagactttggggtaatagcaacctttgacc 862

Db 810 ccaaaccatccctgggaactggaacggtgtgctggtgtcacaccaacttcagcaccaaga 869
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Qy 863 ccaagcccatcctgggaactggaatggtgcaggtgccaatacctaactttagcaccaagg 922

Db 870 acatgagggaagatggaggtctcaagcacatcgaggaggccatcgagaagctgagcaagc 929
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Qy 923 ccatgcgggaggagaatggtctgaagcacatcgaggaggccatcgagaaactaagcaagc 982

Db 930 gccaccagtaccacatccgtgcctacgaccccaaggagggtggacaacgcccggcgcc 989
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Qy 983 ggccaccgtaccacattcgagcctacgatcccaagggggcctggacaatgcccggtgtc 1042

Db 990 tgacgggcttccacgagacgtccagcatccacaggttctccgccggcggtggccaaccgcg 1049
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Qy 1043 tgactgggttccacgaaacgtccaacatcaacgacttttctgctggtgtcgccaatcgca 1102

Db 1050 gcgcagcatccgcatccacgcaacgtgggcatgagaagaaaggctacttcaggagacc 1109
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Qy 1223 ttctcaatgagactggcgacgagcccttccaatacaaaaaactaattagact 1273

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Search completed: Fri Aug 8 16:45:36 1997
Job time : 2569 secs.

MOEORU

(TM)

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```
Run on:      Fri Aug  8 16:45:55 1997; MasPar time 133.41 Seconds
           984.006 Million cell updates/sec
Tabular output not generated.
```

Scoring table: TABLE default
Gap 6

```
Post-processing: Minimum Match 0%
                  Listing first 45 summaries
```

Statistics: Mean 9.364; Variance 4.957; scale 1.889

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
	1	1419	100.0	1419	2	N70819	Sequence encoding chi	0.00e+00
	2	1187	83.7	13254	23	T40915	Nucleotide sequence o	0.00e+00
	3	134	9.4	1429	1	N91849	Lettuce glutamine syn	2.62e-79
	4	130	9.2	1255	1	Q05727	Gene encoding glutami	3.03e-76
	5	131	9.2	1649	2	Q10333	Encodes Rice chloropl	5.20e-77
	6	128	9.0	1200	1	Q05728	Gene encoding glutami	1.02e-74
	7	127	8.9	1262	1	Q05729	Gene encoding glutami	5.95e-74
	8	124	8.7	1338	2	N70758	Sequence encoding alf	1.16e-71
	9	122	8.6	1068	2	N71176	Sequence encoding mut	3.86e-70
	10	79	5.6	246	22	T26426	Human gene signature	5.44e-38
	11	76	5.4	1047	2	Q10572	Human Natriuretic Pep	8.29e-36
c	12	77	5.4	1047	2	Q10572	Human Natriuretic Pep	1.56e-36
	13	58	4.1	185	2	N70762	Partial sequence of t	5.56e-23
	14	58	4.1	221	2	N70760	Partial sequence of t	5.56e-23
	15	47	3.3	1200	1	N90907	Glutamine synthesis g	1.84e-15
	16	45	3.2	91	9	Q51746	Oligonucleotide probe	3.93e-14
	17	46	3.2	4464	2	N71244	Genomic sequence of a	8.53e-15
	18	46	3.2	4465	5	Q28697	Glutamine synthetase.	8.53e-15
c	19	43	3.0	91	9	Q51746	Oligonucleotide probe	8.14e-13
c	20	42	3.0	204	1	N81164	Base substituted E.co	3.66e-12
	21	43	3.0	312	2	N70764	Partial sequence of t	8.14e-13
	22	41	2.9	204	1	N81164	Base substituted E.co	1.63e-11
	23	37	2.6	348	6	Q39897	Expressed Sequence Ta	5.78e-09
	24	37	2.6	348	8	Q59309	Human brain Expressed	5.78e-09
	25	36	2.5	114	12	Q70467	Generic DNA sequence	2.44e-08
	26	34	2.4	48	18	T13986	Glutamine synthetase	4.19e-07

27	34	2.4	114	12	Q70468	Generic DNA sequence	4.19e-07
28	34	2.4	114	12	Q70465	Generic DNA sequence	4.19e-07
29	33	2.3	114	12	Q70470	Generic DNA sequence	1.70e-06
30	32	2.3	114	12	Q70472	Generic DNA sequence	6.80e-06
31	32	2.3	114	12	Q70469	Generic DNA sequence	6.80e-06
c 32	32	2.3	114	12	Q70469	Generic DNA sequence	6.80e-06
c 33	32	2.3	114	12	Q70468	Generic DNA sequence	6.80e-06
34	33	2.3	200	2	N70759	Partial sequence of t	1.70e-06
35	31	2.2	114	12	Q70471	Generic DNA sequence	2.68e-05
c 36	31	2.2	114	12	Q70467	Generic DNA sequence	2.68e-05
37	30	2.1	114	12	Q70466	Generic DNA sequence	1.04e-04
c 38	30	2.1	114	12	Q70470	Generic DNA sequence	1.04e-04
c 39	30	2.1	114	12	Q70465	Generic DNA sequence	1.04e-04
c 40	30	2.1	501	3	N50023	Sequence encoding new	1.04e-04
41	29	2.0	114	12	Q70473	Generic DNA sequence	3.95e-04
c 42	29	2.0	114	12	Q70466	Generic DNA sequence	3.95e-04
c 43	28	2.0	501	3	N50026	Sequence encoding new	1.48e-03
c 44	28	2.0	501	3	N50033	Sequence encoding new	1.48e-03
c 45	26	1.8	114	12	Q70471	Generic DNA sequence	1.94e-02

ALIGNMENTS

RESULT 1

ID N70819 standard; cDNA; 1419 BP.

AC N70819;

DT 13-MAY-1991 (first entry)

DE Sequence encoding chinese hamster glutamine synthetase.

KW DHER/MTX; ss.

OS Cricetulus griseus.

FH Key Location/Qualifiers

FT stem_loop 7..80

FT /*tag= a

FT stem_loop 81..130

FT /*tag= b

FT CDS 145..1266

FT /*tag= c

PN WO8704462-A.

PD 30-JUL-1987.

PF 23-JAN-1987; GO0039.

PR 23-JAN-1986; GB-001597.

PA (CELL-) CELLTECH LTD.

PA (UNIU) UNIV OF GLASGOW.

PA (WILS/) WILSON RH.

PI Wilson RH, Bebbington CR;

DR WPI; 87-221263/31.

DR P-PSDB; P70501.

PT Recombinant DNA which encodes glutamine synthetase - used esp. in

PT co-amplification of non-selected genes and in transforming host

PT cell lines.

PS Claim 6; Fig 2a-e; 54pp; English.

CC Sequence may be used as a hybridisation probe in the isolation of the

CC GS gene in other species, and as a diagnostic tool in the detection

CC of diseases altering GS expression. A second use is as a selectable

CC marker in recombinant DNA technology eg. co-amplification selection,

CC or transformation to glutamine independence.

SQ Sequence 1419 BP; 338 A; 391 C; 361 G; 329 T;

Query Match 100.0%; Score 1419; DB 2; Length 1419;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 1419; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1	ccgagccgagaatgggagtagagccgactgcttgattcccacaccaatctcctcgccgct	60
Qy	1	ccgagccgagaatgggagtagagccgactgcttgattcccacaccaatctcctcgccgct	60
Db	61	ctcaattcgctcgttctcgtggctcgtggccctgtccaccccgccatcatcccgccg	120
Qy	61	ctcaattcgctcgttctcgtggctcgtggccctgtccaccccgccatcatcccgccg	120
Db	121	ccaccgctcagagcaccttcaccatggccacctcagcaagttccactgaacaaaaac	180
Qy	121	ccaccgctcagagcaccttcaccatggccacctcagcaagttccactgaacaaaaac	180
Db	181	atcaagcaaatgtactgtgcctgccccagggtgagaaagtcgaagccatgtatatctg	240